

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 16, 2003, 16:55:57 : Search time 110.214 seconds  
(without alignments)  
330.553 Million cell updates/sec

Title: US-09-856-070-18  
Perfect score: 24  
Sequence: 1 KEELM 5

Scoring table: BLOSUM62  
Xgapop 10.0 ; Xgapext 0.5  
Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 ; Fgapext 7.0  
helop 6.0 ; helext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4105280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n model -DEV=zip  
-Q=/cdm2-1/USPTA\_spool/US09856070/runat\_14012004\_155834\_1621/app\_queryfasta\_11592  
-DB=GenEmbl -GEMT=fastap -SUFFIX=rge -MINMATCH=0.1 -DEOPT=0 -LOOPTXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LSP=45  
-DOCALLIGN=200 -LHR\_S20KEXT=1 -LHR\_MAX=100 -LHR\_MIN=0 -ALPH=15 -MODE=LOCAL  
-OUTFMT=plc -NPM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856070 -ALN=1 -CVAL=runat\_14012004\_155834\_1621 -NPM=F -L=PH-A  
-N7\_XLPXY -NO\_MMAPP -LAPQUERY -NEV\_SCORES=0 -WAIT -LNNBLW -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THRPADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database :

GenEmbl :  
1: gb\_ba :  
2: gb\_hig :  
3: gb\_in :  
4: gb\_om :  
5: gb\_ov :  
6: gb\_pat :  
7: gb\_ph :  
8: gb\_pl :  
9: gb\_pr :  
10: gb\_ro :  
11: gb\_sts :  
12: gb\_sv :  
13: gb\_un :  
14: gb\_vl :  
15: om\_ba :  
16: om\_fun :  
17: om\_hum :  
18: om\_in :  
19: om\_mu :  
20: om\_om :  
21: om\_or :  
22: om\_ov :  
23: om\_ph :  
24: om\_pl :  
25: om\_ro :  
26: om\_sts :  
27: om\_un :  
28:

29: om\_vl :  
30: em\_hig\_hum :  
31: em\_hig\_inv :  
32: em\_hig\_other :  
33: em\_hig\_mus :  
34: em\_hig\_pin :  
35: em\_hig\_rnd :  
36: em\_hig\_mam :  
37: em\_hig\_vrt :  
38: em\_sy :  
39: em\_hig\_hum :  
40: em\_hig\_mus :  
41: em\_hig\_other :

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	24	100.0	30	6	AK024524
C 2	24	100.0	22	6	AK053145
C 3	24	100.0	75	5	AF033542
C 4	24	100.0	77	6	A25925
C 5	24	100.0	77	6	A25926
C 6	24	100.0	128	9	HS195C10F
C 7	24	100.0	129	9	HS195C10F
C 8	24	100.0	162	9	HSLAS80B
C 9	24	100.0	195	9	HSU55185
C 10	24	100.0	226	11	GL16198
C 11	24	100.0	242	9	HSAL11611
C 12	24	100.0	348	3	AF082538
C 13	24	100.0	348	11	AF082715
C 14	24	100.0	351	11	HSPH1802
C 15	24	100.0	352	11	G25533
C 16	24	100.0	354	11	G25536
C 17	24	100.0	362	6	AX337439
C 18	24	100.0	371	11	HSB3082E9
C 19	24	100.0	372	3	AF152580
C 20	24	100.0	377	1	AF336818
C 21	24	100.0	384	11	G17562
C 22	24	100.0	396	6	AX071771
C 23	24	100.0	399	6	AX071365
C 24	24	100.0	410	3	AF390903
C 25	24	100.0	426	5	AF306569
C 26	24	100.0	431	9	HUMSP25
C 27	24	100.0	438	11	G28129
C 28	24	100.0	453	6	AX392765
C 29	24	100.0	460	9	AF190059
C 30	24	100.0	471	9	AF188896
C 31	24	100.0	472	3	AF095204
C 32	24	100.0	475	9	AF188897
C 33	24	100.0	478	9	AF189213
C 34	24	100.0	489	9	AF187552
C 35	24	100.0	507	14	VVLLENV
C 36	24	100.0	508	8	AF482638
C 37	24	100.0	523	11	G20947
C 38	24	100.0	539	6	AX106210
C 39	24	100.0	539	6	AX106529
C 40	24	100.0	539	6	AX140820
C 41	24	100.0	539	6	AX205680
C 42	24	100.0	539	6	AX267336
C 43	24	100.0	542	6	AX046513
C 44	24	100.0	544	11	G58413
C 45	24	100.0	545	6	AX387845

ALIGNMENTS

RESULT 1



```

Alignment Scores:
Pred. No.: 99.6 Length: 77
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-18 (1-5) x A25926 (1-77)
QY 1 LysGluGluLeuMet 5
DB 23 AACGACCAATTAATG 9

RESULT 5
A25926 A25926 77 bp DNA linear PAT 06-MAR-1995
DEFINITION MXXX promoter sequences.
ACCESSION A25926
VERSION A25926.1 GI:833683
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
    source
        location/Qualifiers
            1..77
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                13 q 19 t

BASE COUNT 36 a 9 c 13 q
ORIGIN
    128 bp DNA linear PAT 19-OCT-1995
    H.sapiens Cpg island DNA genomic MseI fragment, clone 195c10,
    reverse read cpg195c10.ftla.

Alignment Scores:
Pred. No.: 99.6 Length: 77
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-18 (1-5) x A25926 (1-77)
QY 1 LysGluGluLeuMet 5
DB 59 AACGACCAATTAATG 73

RESULT 6
HS195C10F/C
LOCUS
DEFINITION H.sapiens Cpg island DNA genomic MseI fragment, clone 195c10,
forward read cpg195c10.ftla.
ACCESSION 260206
VERSION 260206.1 GI:1032110
KEYWORDS Cpg island; genomic MseI fragment.
SOURCE Cpg island; genomic MseI fragment.
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
    1 (bases 1 to 128)
    Submitted (16 OCT 1995) The Sanger Centre, Hinxton, Cambridgeshire,
    CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 128)
AUTHORS Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
TITLE Purification of Cpg islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE 94282070
PUBMED 8012384
COMMENT Vector: pCEM-52f(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.

FEATURES
    source
        location/Qualifiers
            1..128
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="195c10"
                /sex="male"
                /tissue_type="blood"
                /clone_lib="CGI-1"
                /dev_stage="adult"
                23 q 39 t 3 others

BASE COUNT 54 a 10 c 23 q
ORIGIN
    Alignment Scores:
    Pred. No.: 160 Length: 129
    Score: 24.00 Matches: 5
    Percent Similarity: 100.00% Conservative: 0
    Best Local Similarity: 100.00% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 9 Gaps: 0

US-09-856-070-18 (1-5) x HS195C10F (1-128)
QY 1 LysGluGluLeuMet 5
DB 76 AAAGAGCAATTCATG 62

RESULT 7
HS195C10R
LOCUS
DEFINITION H.sapiens Cpg island DNA genomic MseI fragment, clone 195c10,
reverse read cpg195c10.ftla.
ACCESSION 260207
VERSION 260207.1 GI:1032110
KEYWORDS Cpg island; genomic MseI fragment.
SOURCE Cpg island; genomic MseI fragment.
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
    1 (bases 1 to 129)
    Submitted (16 OCT 1995) The Sanger Centre, Hinxton, Cambridgeshire,
    CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 129)
AUTHORS Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
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http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.

FEATURES
    source
        location/Qualifiers
            1..129
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="195c10"
                /sex="male"
                /tissue_type="blood"
                /clone_lib="CGI-1"
                /dev_stage="adult"
                23 q 39 t 3 others

BASE COUNT 54 a 10 c 23 q
ORIGIN
    Alignment Scores:
    Pred. No.: 160 Length: 129
    Score: 24.00 Matches: 5
    Percent Similarity: 100.00% Conservative: 0
    Best Local Similarity: 100.00% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 9 Gaps: 0

```







Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 11 Gaps: 0

US-09-856-070-18 (1-5) x G25533 (1-352)

QY 1 LysGluGluLeuMet 5

|||||

DB 134 AAGGAAGAGCTCATG 148

Search completed: January 16, 2003, 19:02:40  
Job time : 442.214 secs

